



**Figure 2**

**Sialidase**

**Hydrolysis of donor boded silalic acids**



**Sialyltransferase**

**Transfer of sialic acids activated with C M P to acceptor molecules**



**Trans-sialidase**

**Transfer of sialic acids from donor to acceptor molecules**



### Figure 3

T.r.s : ~~~~~\*~~~~~20~~~~~\*~~~~~40~~~~~\*~~~~~60~~~~~\*~~~~~80~~~~~\*~~~~~100~~~~~\*~~~~~120~~~~~: 44  
 T.cr.TS : ~~~~~MGKTIVGASRMFWLMEFVPELLLALCPSEPAHALAGSSRVELFKRSSKVPF-E : 53  
 T.b.br.TS : MEELHQMRMPISRLLLIPTAVCHCCALTSKAAGKGTREAFISGGAWALRKLSKDKGEVWVWQDGNWKKDYDKEWERWKEEKGPGGSEKRSEWFAHMTGGYITLGKTKILSSAIE : 120  
 T.con.TS1 : ~~~~~- : -  
 T.con.TS2 : ~~~~~- : -  
  
 T.r.s : ~~~~~\*~~~~~140~~~~~\*~~~~~160~~~~~\*~~~~~180~~~~~\*~~~~~200~~~~~\*~~~~~220~~~~~\*~~~~~240~~~~~: 160  
 T.cr.TS : KGGKVTERRVHSHRLALUNYDSMVVALABARETENNBLISTVARIYVLDGEFMEBQALAKHS-RASSVSPVVDTEIVVNGNKLYLVGSSNRSSTQTHSGD---ARQNDILLAVSE : 169  
 T.b.br.TS : GSDKV-ERTVHSHRLISTEPVDEYLMGIGARMLTSTYFFTTSTVARIYSAAGGKTQKREVTIENGCRVDPITYSPVVDSTVVAADSVFVWARINVTRGYNHNETNAAGIAQEPFMYKEV : 239  
 T.con.TS1 : ~~~~~TETVAKISDGRCTQKREVTIENGCRVDAHSEVMDSTVVAKENIYVAGRIINVTRGYNHNRNNKAGIADQEPFYKET : 79  
 T.con.TS2 : ~~~~~DRIISLLEIDVYLIAFFDRLRASLSSLIETAMKYSANQCKTKKLEIILKHARITDNFRRVMDSTVVAQNDLIFVGRMTSSAPVWQEN---GRKQDVLLYKAK : 105  
  
 T.r.s : ~~~~~\*~~~~~260~~~~~\*~~~~~280~~~~~\*~~~~~300~~~~~\*~~~~~320~~~~~\*~~~~~340~~~~~\*~~~~~360~~~~~: 272  
 T.cr.TS : YTHSAAGKTTATSECKP--VSKPLFPAPFDFGLTKREHIGVAAALVGSYNLYVGVQIADMGGRRVTKIMSEBGGNTAKAEARSKFCEBPAAVLBBGKLLINNRVGN----- : 281  
 T.b.br.TS : YTHSAAGKITASEKFGSD--VSKKEFPAPMECPMHTNBGLSAGVAIVASINENLYVPAVTNKKKKQVFKKPYSEBEBTKKSGEGRSDPFCSEBPAAVLBBGKLLINNRVGN----- : 281  
 T.b.br.TS : YTHGADGKTSVDRSETKTKPLKPYDEIVAGSKF---TBBHGAAGNGVFLNGTLFPLPQARNEDNAVSHVMVYVBBGVSHHARDETALLTSEASLTENAGLINSARTTSGVNVBG : 356  
 T.con.TS1 : YNVGTRENATDVSSEKERTALKSEYNEPVSGSPS---TBBHGAAGGVVTSNCTILLEVQARNKANRVEMILYBADDKSTHGGKSEAGVETSEAAITSDGSKLLISAPSSGG---Q : 191  
 T.con.TS2 : YRRESAGVVPVSFTDDELYLKHLLTVGKIDPERSLITVYSEVNGCLVTPKGTILFVGVQVLTNKSNNMLLYSSNCKTDEGSKTSPARTTSEASLYVMDGKLLITSETTPD---V : 220  
  
 T.r.s : ~~~~~\*~~~~~380~~~~~\*~~~~~400~~~~~\*~~~~~420~~~~~\*~~~~~440~~~~~\*~~~~~460~~~~~\*~~~~~480~~~~~: 383  
 T.cr.TS : -RLMAYESBDEKTAIVALETLGHVTTQSTISNOO---D-COSSEVAVTHSGKRNILFTHPLNKGRRNRDRNHLMMNNORIFDVEGHTTBBNGSGSEVHYKD-KIMSHHEIT : 392  
 T.b.br.TS : -RLMAYESBDEKTAIVALETLGHVTTQSTISNOO---G-SOSSEITAHTSGKRNILFTHPLNKGRRNRDRNHLMMNNORITYNVEGVTIETBNAGSEVHYKDS-KIMSHHEIT : 392  
 T.b.br.TS : GFRKMPESNNKCATDESLISTSVIENSDDRTKSTPTANYPGSSGALITLGDGVVHLITHEKNTKANSRDRDQVWMDGNGMVLGCTIETBBDNSAKSGLLARSGLVGHERRI : 476  
 T.con.TS1 : GYHPIPESSDLATKREMLNSISRVICUSGKSG---G-SSSGEITLVVGEVPHILTHEDKLLGSYYQRYQOLMMGNGMHHVGVSEBDNSAKSGLLARSGLVGHERRI : 304  
 T.con.TS2 : GSRPHTLSDTSTSEALTSIRSVIENSRYRND---G-GSGSIAIVSGVPHILTHG--- : 277  
  
 T.r.s : ~~~~~\*~~~~~500~~~~~\*~~~~~520~~~~~\*~~~~~540~~~~~\*~~~~~560~~~~~\*~~~~~580~~~~~\*~~~~~600~~~~~: 502  
 T.cr.TS : NDGVSVFVRFGSGQMLKSVVRTREEDNHASISTEVVPATPESKQCGAAVETADIVCFSHSANGSVTEVMSDQNVANAEVFNELKENGVCSS-AVFNARAGSTRWOSAN : 511  
 T.b.br.TS : NDGVSVFARLVGSRITKSVLOSITNNSSHSSISTPADPAASSSEREGPAVTHVCFVSHSATKTEBKAERENSTANAEVFNELKFAVGCGG-ALHNSOSSEGNORHGAN : 592  
 T.b.br.TS : DEYSHHLVHLVDSEKYNATVRKJDAOSALAGLSSSRKKNDPTCSG---VDDSHVHLVAGPVGASVAAVMDGNVNSISDGVKYSEVQLGKKRNSRVLENSBEGDQDQRYBAN : 419  
 T.con.TS1 : DEYSHHLVRLVDSEKSIKSTALVYHACLELNLGNLEGG-DKYDSCDG---IETADIVAVGPTETKTPAARENATSGAVSTAEVRLDVGCGGHVHVVSESGSDQRYBAN : 419  
 T.con.TS2 : ~~~~~- : -  
  
 T.r.s : ~~~~~\*~~~~~620~~~~~\*~~~~~640~~~~~\*~~~~~660~~~~~\*~~~~~680~~~~~\*~~~~~700~~~~~\*~~~~~720~~~~~: 620  
 T.cr.TS : YRDEAVATITIDELKGTSSRLAGLEGPGDAKLGLSEYDKNRQRLPLKGAAP-ASPTGSEWLHKHYVVTMAADRGSSVYVDQPLAGSGNTVVRGA-TLPDISHEYIIGPRSKGAPTD : 629  
 T.b.br.TS : HAPNVASITHEVGSVASPLASLSDSSGGKLLGLSEYDEKHQHOPIKSTP-VTPTGSEWEGKRYHYVTMAKNGISVYIDGPLEGSGQTVVPDG-RTPDISHEYIYVGGYGRSDMPTI : 711  
 T.b.br.TS : THPLLATRFAGEKAEADMPFSAEGKTSSETSLTVGGK-KVLTIGSVRKEGPTTMDWNQHQIAELRLRGKVDHVNGLIKEVBSVGAESSAHLHLSEHFIAPVNDSGEGG : 497  
 T.con.TS1 : SEDEAVTTRFDEMGELELLEFVNRKGVKIKRVLESGV-EILLAKNGEYNSTAAEPLDVNESHQVYALHGTVE : -  
 T.con.TS2 : ~~~~~- : -  
  
 T.r.s : ~~~~~\*~~~~~740~~~~~\*~~~~~760~~~~~\*~~~~~780~~~~~\*~~~~~800~~~~~\*~~~~~820~~~~~\*~~~~~840~~~~~: 660  
 T.cr.TS : SRVTVNIVLYNRRINSSEIRTEFLSQDMITGDDGAGTAA- : 749  
 T.b.br.TS : SHVTVNIVLYNRRQLNAEIBIRTEFLSQDLGTEAHMGSSSGSSAHSTPSTPADNGAHSTPSTPADSSAHSTPSTPADSSAHSTPSAPGDNGAHSTPSTPGDSSAHSTPSTPADNGAHSTP : 831  
 T.con.TS1 : ~~~~~- : -  
 T.con.TS2 : ~~~~~- : -  
  
 T.r.s : ~~~~~\*~~~~~860~~~~~\*~~~~~880~~~~~\*~~~~~900~~~~~\*~~~~~920~~~~~\*~~~~~940~~~~~\*~~~~~960~~~~~: -  
 T.cr.TS : SAPADSSNAHSTPSTPADNGAHSTPSTPADNGAHSTPSTPGDNGAHSTPSTPGDSSAHSTPSTPADNGAHSTPSAPADSSNAHSTPSTPGDNGAHSTPSAPADSSNAHSTPSTPADSSAHSTP : 869  
 T.b.br.TS : CVLFCVDALRL-TGMVAEVARWDPSPALTYGSSPPSIRTESAT- : 874  
 T.con.TS1 : ~~~~~- : -  
 T.con.TS2 : ~~~~~- : -  
  
 T.r.s : ~~~~~\*~~~~~980~~~~~\*~~~~~1000~~~~~\*~~~~~1020~~~~~\*~~~~~1040~~~~~\*~~~~~1060~~~~~\*~~~~~1080~~~~~: -  
 T.cr.TS : SAPGDNGAHSTPSAPADSSAHSTPSAPGDNGAHSTPSAPADNGAHSTPSAPGDSSAHSTPSTPADSSAHSTPSTPADSSAHSTPSAPGDNGAHSTPSAPADSSAHSTPSTPGDSSAHSTP : 989  
 T.b.br.TS : ~~~~~- : -  
 T.con.TS1 : ~~~~~- : -  
 T.con.TS2 : ~~~~~- : -  
  
 T.r.s : ~~~~~\*~~~~~1100~~~~~\*~~~~~1120~~~~~\*~~~~~1140~~~~~\*~~~~~: -  
 T.cr.TS : SAPADSSAHSTPSAPGDNGAHSTPSTPADNGANGTVLLIHDGAAPSAFSGGGLLCAGALLHVVMVAVFF-- : 1060  
 T.b.br.TS : ~~~~~- : -  
 T.con.TS1 : ~~~~~- : -  
 T.con.TS2 : ~~~~~- : -